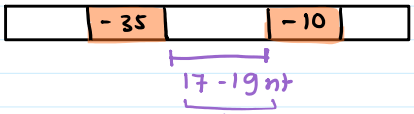
Mechanism of Transcription [Prokaryote]

Transcription completed in 3 step -

(i) Initiation
(ii) Elongation
(iii) Termination

(i) Initiation

- σ Factor play imp. role in initiation process.
  - ↳ Recognize [-10 & -35 seq.]

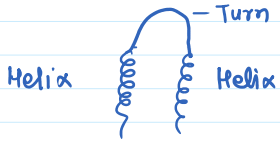


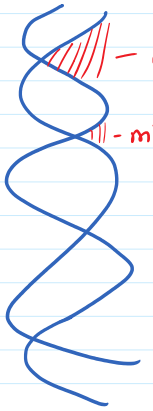
distance b/w these 2 seq. = Strong promotor

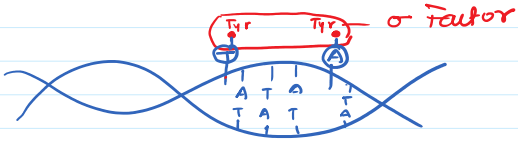
if distance vary b/w these 2 seq. → Promotor become weak

σ Factor

- Structure ⇒ Helix - Turn - Helix
  - ↓
  - Binds with major groove of DNA at only -35 & -10 seq.







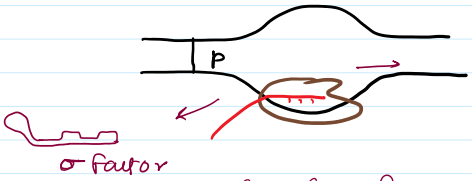
σ Factor - Contain aromatic a.a.

- Interacts with Backbone of DNA
  - ↓
- melting of H Bond b/w A & T
  - ↓
  - Steric change
  - ↓
  - More H Bond melting start at pribnow Box

↓

Transcription bubble formation

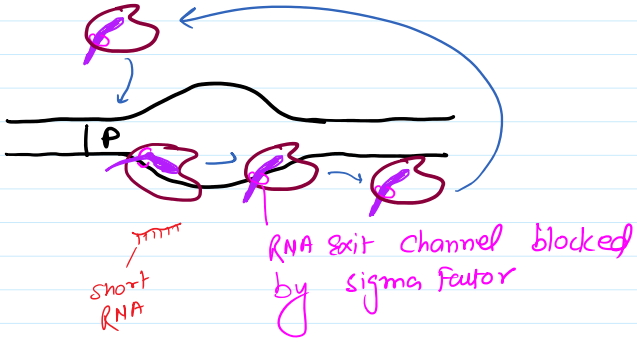
[12 - 14 nt melt]



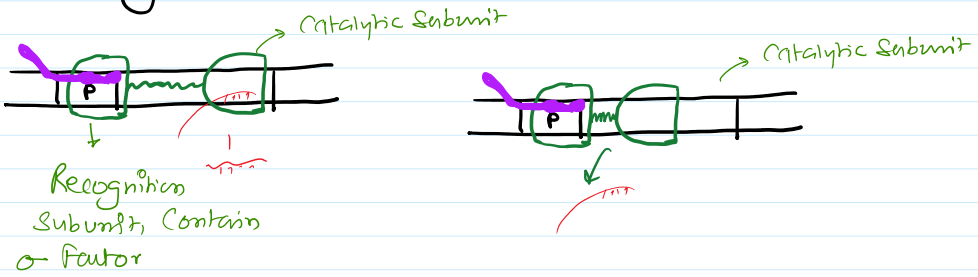
dissociates & RNA Pol. moves forward → Elongation start

Before Elongation RNA Pol. Shows Abortive Round of Transcription

① Transient excursion model [local excursion model]



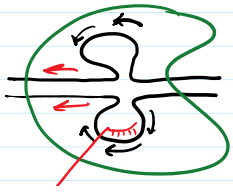
② Inch warming model

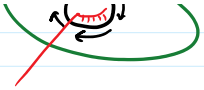


③ Scrunching model

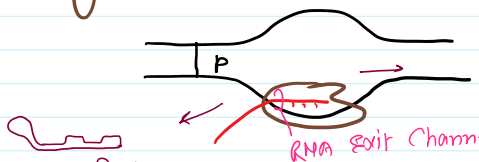
- RNA Pol. does not moves along DNA Thread

-> DNA Thread itself moves through RNA Pol. for Transcription





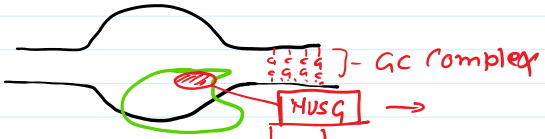
* if σ factor Removed from RNA Pol. [Promoter escape]
↓
Elongation Start



σ factor dissociates & RNA Pol. moves forward → Elongation start

(2) Elongation

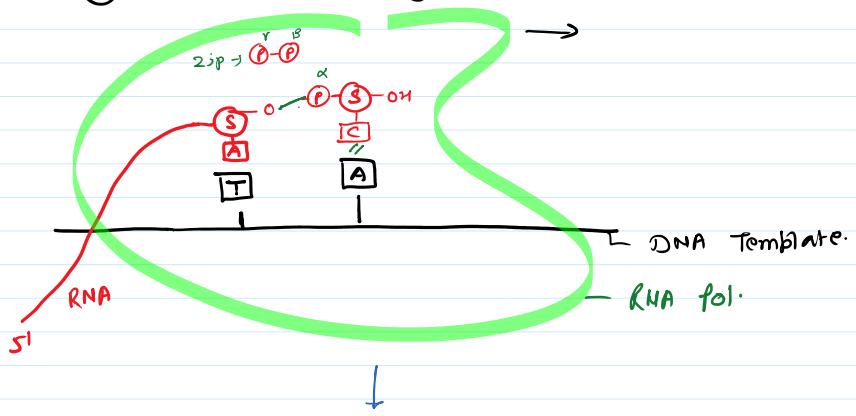
- σ factor removed from Promoter
- (NUS G) Protein +nt with RNA Polymerase
  ↓
  Prevent Closing of open Complex



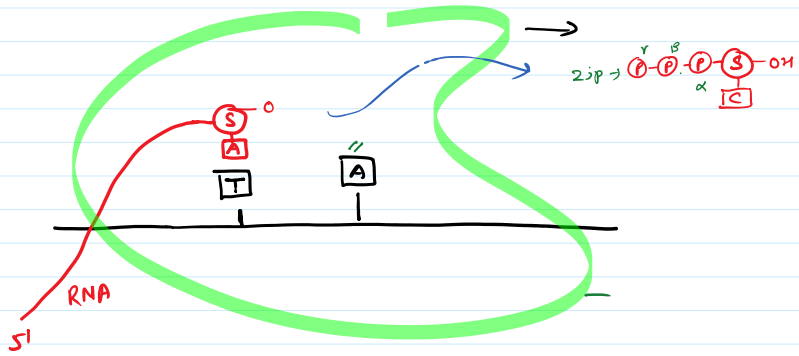
- Prevent Closing of open Complex
- → Conserve in all 3 domain of life
- → SPT-5 is Homolog of Hus-G in Eukaryote

Proof reading in RNA Polymerase

(1) Pyrophosphate editing -



↓



if there is mismatch during Transcription
Pyrophosphate attack on phosphodiester bond
of wrong Base of RNA

If there is Damage in DNA strand during Transcription
↓
Transcription Coupled Repair System
works
- Transcription Coupled Releasing factor [TCRF]
Enters in Transcription Complex
UvrABC → RNA Pol. Removed
Repair

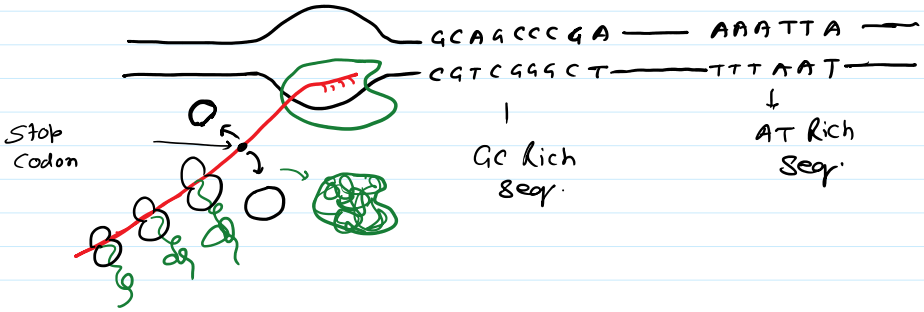
(ii) Hydrolytic cleavage
- mismatch nt. Cleaved by (Gre) - in Prokaryote
T.F. II S is Homolog of GRE in Eukaryote

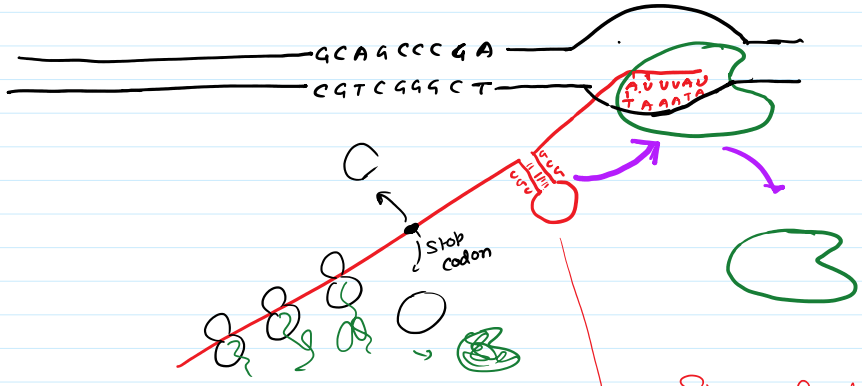
(3) Termination
(1) Rho – independent
(2) Rho – dependent [Prokaryote]

(1) Rho - independent termination [most common]

① Rho - independent termination [most common]

↳ also k/a Intrinsic Termination





→ Stem loop

- Cause Termination of Transcription

① Stem-loop str. brings Allosteric change in RNA Pol.

↓

- RNA Pol. dissociates from Template & Transcript Release

② RNA Pulled from Transcription Bubbles → Transcription bubble closed

③ Torpedo model

- Hair pin loop - Push Forword RNA Pol.

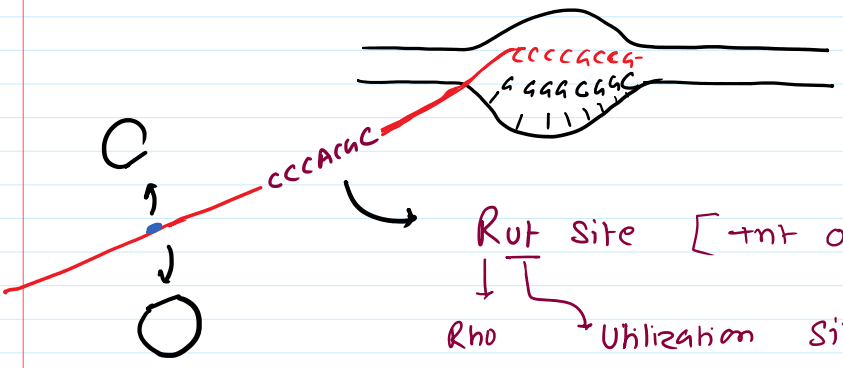
↓

RNA Pol. dissociates from Transcription bubble

↓
Transcript Released.

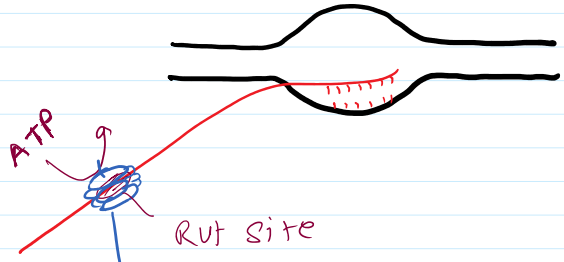
* Xrn 2 in human & Rat 1 in yeast
↓
helps in dissociation of RNA Transcript from Transcription bubble in Eukaryotic Transcription Termination

(ii) Rho dependent Termination [in Some Bacterial sp.]
↓
Via Extrinsic Termination



Rut Site [mRNA on RNA Transcript]
↓
Rho Utilization Site [C Rich seq.]

- Recruit Rho Factor
  - 6 Subunit
  - ATPase activity mRNA



Rho Factor [Extrinsic Factor]
① Brings Allosteric Change in RNA Pol.

(ii) Push forward RNA Pol.

(iii) Enters in Transcription bubbles & disrupt H Bond b/w RNA & DNA

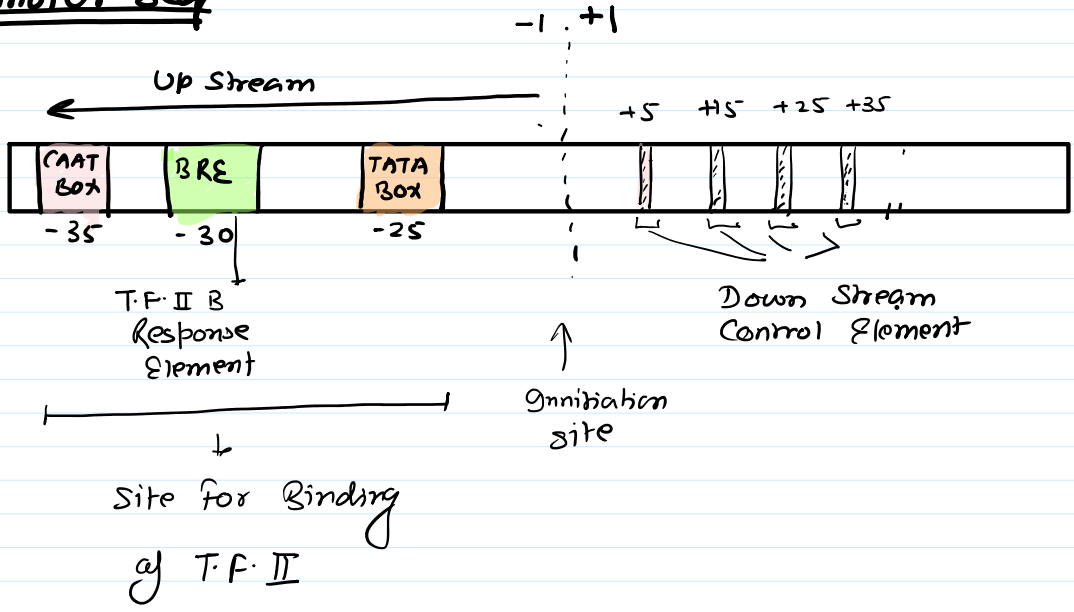
Open Complex → Close Complex

Eukaryotic Transcription

- RNA Pol. II → Transcription of protein coding gene

RNA Pol. II + General Transcription factor
(T.F. II. A, B, D, E, F, H)

Promoter Seq.



In Eukaryote - Transcription and Translation is seperated by space and time

Transcription site = Nucleus

Translation site = Cytoplasm

Co-Transcriptional Event

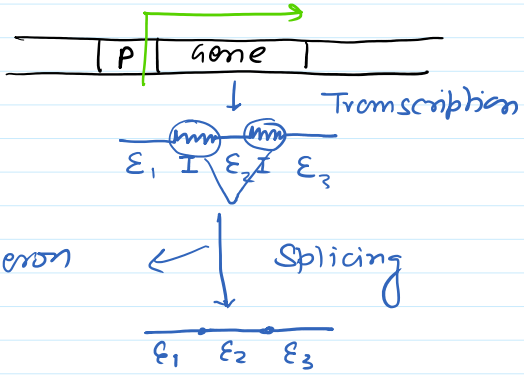
- 5' Capping
- 3' tailing

Post Transcriptional Event

- Splicing
  - Removal of intron & joining of Exon

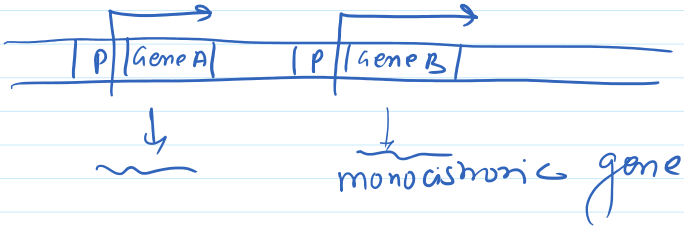
in Eukaryotes - there is Split gene is not

Contain Exon & intron seq.



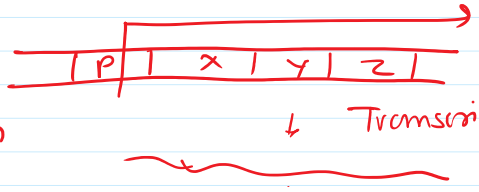
in Eukaryotes - Transcription is mono-cistronic

Each gene contain its own promoter



in Prokaryote Polycistronic gene is common

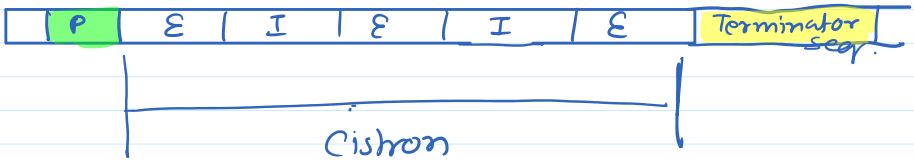
eg. lac operon



↓

* Basal Rate of Transcription in Eukaryote = 40 nt/sec

- Speed of Transcription is fixed but frequency could changed



Avarage size of agene in human = 27 Kb

Avarage Exon No. = 9

Avarage Exon Size = 150 bp

Total Exon Size = 9 x 150 = 1350 bp

Avarage Interon No. = 8

each Interon Size = 3000 bp

Total Interon Size = 8 x 3000 = 24,000 bp

Smallest gene = H_1 Histone (interon-nt)

Largest gene = Dystropin (100 interon)

Largest Protein = titin

DNA Seq. 5'-ATGCTCA-3' Template

3'-UACGAGU-5' mRNA

1

3rd option is correct